

SEQUENCE LISTING

<110> COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

<120> Polyphenol oxidase genes from banana, lettuce, tobacco and
pineapple

<140>

<141>

<150> US 08/976, 222

<151> 1997-11-21

<150> PCT/AU98/00362

<151> 1998-05-19

<150> AU PP3898

<151> 1995-05-23

<150> AU PP6849

<151> 1997-05-19

<150> AU PP5600

<151> 1995-09-26

<160> 49

<170> PatentIn Ver. 2.0

<210> 1

<211> 582

<212> DNA

<213> banana

<220>

<221> CDS

<222> (1)..(582)

<400> 1

cac tgt gcg tat tgt gat ggc gcc tac gac cag atc ggc ttc ccc aac 48

His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asn

1 5 10 15

ctc gag ctc caa gtc cac aac tcc tgg ctc ttc ttc cct tgg cac cgc 96

Leu Glu Leu Gln Val His Asn Ser Trp Leu Phe Phe Pro Trp His Arg

20 25 30

ttc tac ctc tac ttc cac gag agg atc ctc gga aag ctc ata ggc gac 144

Phe Tyr Leu Tyr Phe His Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp

35 40 45

gac act ttc gcc ctc cct ttc tgg aac tgg gac gcg ccc ggc ggc atg 192

Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met

50	55	60	
aag ctg ccg tcg atc tac gcc gac cct tcg tcc tcg ctc tat gac aag			240
Lys Leu Pro Ser Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys			
65	70	75	80
ttt cgc gac gcc aag cac cag ccg cca gtc ctc gtc gac ctc gac tac			288
Phe Arg Asp Ala Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr			
85	90	95	
aac gga acc gac cct agt ttc acc gac gca gag cag atc gat cag aac			336
Asn Gly Thr Asp Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn			
100	105	110	
ctc aag atc atg tac cgg cag gtg atc tcc aac ggc aag acg ccg ttg			384
Leu Lys Ile Met Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu			
115	120	125	
ctc ttc tta ggc tcg gct tac cgt gcc ggc gac aac cca aac ccc ggc			432
Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly			
130	135	140	
gcg ggc tcg ctc gag aac ata cca cac ggc ccc gtc cac ggg tgg act			480
Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr			
145	150	155	160
ggc gac aga agc caa ccc aat ctc gag gac atg ggc aac ttc tac tcc			528
Gly Asp Arg Ser Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser			
165	170	175	
gcg ggg cgc gac cct atc ttc ttc gcc cac cat tca aat gtc gat cgc			576
Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg			
180	185	190	
atg tgg			582
Met Trp			

<210> 2

<211> 194

<212> PRT

<213> banana

<400> 2

His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asn

1

5

10

15

Leu Glu Leu Gln Val His Asn Ser Trp Leu Phe Phe Pro Trp His Arg

	20		25		30
Phe Tyr Leu Tyr Phe His Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp					
	35		40		45
Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met					
	50		55		60
Lys Leu Pro Ser Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys					
	65		70		75
					80
Phe Arg Asp Ala Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr					
		85		90	95
Asn Gly Thr Asp Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn					
	100		105		110
Leu Lys Ile Met Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu					
	115		120		125
Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly					
	130		135		140
Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr					
	145		150		155
					160
Gly Asp Arg Ser Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser					
		165		170	175
Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg					
	180		185		190
Met Trp					

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 <212> DNA
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<220>
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 <222> (1)... (426)

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Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Lys Leu Pro Ser
 1 5 10 15

atc tac gcc gac cct tgc tcc tgc ctc tat gac aag ttt cgc gac gcc 96
 Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys Phe Arg Asp Ala
 20 25 30

aag cac cag ccg ccg gtc ctc gtc gac ctc gac tac aac gga acc gac 144
 Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp
 35 40 45

cct agt ttc acc gac gca gag cag atc gat cag aac ctc aag atc atg 192
 Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn Leu Lys Ile Met
 50 55 60

tac cgg cag gtg atc tcc aac ggc aag acg ccg ttg ctc ttc tta ggc 240
 Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu Leu Phe Leu Gly
 65 70 75 80

tgc gct tac cgt gcc ggc gac aac cca aac ccc ggc gcg ggc tgc ctc 288
 Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly Ala Gly Ser Leu
 85 90 95

gag aac ata cca cac ggc ccc gtc cac ggg tgg act ggc gac aga agc 336
 Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr Gly Asp Arg Ser
 100 105 110

caa ccc aat ctc gag gac atg ggc aac ttc tac tcc gcg ggg cgc gac 384
 Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser Ala Gly Arg Asp
 115 120 125

cct atc ttc ttc gcc cac cat tca aat gtc gat agc atg tgg 426
 Pro Ile Phe Phe Ala His His Ser Asn Val Asp Ser Met Trp
 130 135 140

<210> 4

<211> 142

<212> PRT

<213> banana

<400> 4

Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Lys Leu Pro Ser
 1 5 10 15

Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys Phe Arg Asp Ala
 20 25 30

Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp
35 40 45

Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn Leu Lys Ile Met
50 55 60

Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu Leu Phe Leu Gly
65 70 75 80

Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly Ala Gly Ser Leu
85 90 95

Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr Gly Asp Arg Ser
100 105 110

Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser Ala Gly Arg Asp
115 120 125

Pro Ile Phe Phe Ala His His Ser Asn Val Asp Ser Met Trp
130 135 140

<210> 5

<211> 925

<212> DNA

<213> banana

<220>

<221> CDS

<222> (2) .. (853)

<400> 5

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Leu Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro
1 5 10 15

ggc gcg ggc tcg ctc gag aac ata cca cac gcc ccc gtc cac ggg tgg 97
Gly Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp
20 25 30

act ggc gac aga aac caa ccc aat ctc gag gac atg gcc aac ttc tac 145
Thr Gly Asp Arg Asn Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr
35 40 45

tcc gcg ggg cgc gac cct atc ttc ttc gcc cac cat tca aac gtc gac 193
Ser Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp

50	55	60	
cgc atg tgg tac ttg tgg aag aag ctc ggc ggg aag cat cag gac ttt			241
Arg Met Trp Tyr Leu Trp Lys Lys Leu Gly Gly Lys His Gln Asp Phe			
65	70	75	80
aac gat aag gac tgg ctc aac acc acc ttc ctc ttc tac gac gag aat			289
Asn Asp Lys Asp Trp Leu Asn Thr Thr Phe Leu Phe Tyr Asp Glu Asn			
85	90	95	
gct gac tta gtt cga gtc acc ctc aag gac tgc ttg cag ccg gag tgg			337
Ala Asp Leu Val Arg Val Thr Leu Lys Asp Cys Leu Gln Pro Glu Trp			
100	105	110	
ctt cgt tac gat tac caa gac gtc gag atc ccg tgg ctg aag acc cgg			385
Leu Arg Tyr Asp Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Thr Arg			
115	120	125	
ccg act ccc aaa gcc ttg aag gcg cag aaa acc gca gcg aaa aca ctg			433
Pro Thr Pro Lys Ala Leu Lys Ala Gln Lys Thr Ala Ala Lys Thr Leu			
130	135	140	
aaa gct aca gca gag acg ccg ttc ccg gtg acg ctg caa tcc gcg gtg			481
Lys Ala Thr Ala Glu Thr Pro Phe Pro Val Thr Leu Gln Ser Ala Val			
145	150	155	160
agc acg acg gtg agg agg ccc aag gta tcg agg agc ggc aag gag aag			529
Ser Thr Thr Val Arg Arg Pro Lys Val Ser Arg Ser Gly Lys Glu Lys			
165	170	175	
gaa gag gaa gag gag gtc ctc atc gtg gag ggg atc gag ttc gac cgc			577
Glu Glu Glu Glu Glu Val Leu Ile Val Glu Gly Ile Glu Phe Asp Arg			
180	185	190	
gac tac ttc ata aag ttc gac gtc ttc gtg aac gcc acc gag ggt gag			625
Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Glu			
195	200	205	
ggc atc acg ccg ggc gcc agc gag ttc gcg ggc agc ttc gtc aac gtc			673
Gly Ile Thr Pro Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val			
210	215	220	
ccg cac aag cac aag cac agc aag aag gag aag aag ctg aag acg agg			721
Pro His Lys His Lys His Ser Lys Lys Glu Lys Lys Leu Lys Thr Arg			
225	230	235	240
ctc tgc ctg ggg atc act gac ctg ctc gag gac atc ggg gcg gag gac			769
Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp			

245	250	255	
gac gac agc gtg ctc gtc acc atc gtc ccg aaa gcc gga aag ggc aag			817
Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys			
260	265	270	
gtg tgg gtc gcc ggc ctc cgc atc gat ttc cca aat tgaagtaata			863
Val Ser Val Ala Gly Leu Arg Ile Asp Phe Pro Asn			
275	280		
ctatatattt ctactaccta tcaaggaaaa taaaagccgc accatcgtaa caaaaaaaaaa			923
aa			925
<210> 6			
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<212> PRT			
<213> banana			
<400> 6			
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Gly Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp			
20	25	30	
Thr Gly Asp Arg Asn Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr			
35	40	45	
Ser Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp			
50	55	60	
Arg Met Trp Tyr Leu Trp Lys Lys Leu Gly Gly Lys His Gln Asp Phe			
65	70	75	80
Asn Asp Lys Asp Trp Leu Asn Thr Thr Phe Leu Phe Tyr Asp Glu Asn			
85	90	95	
Ala Asp Leu Val Arg Val Thr Leu Lys Asp Cys Leu Gln Pro Glu Trp			
100	105	110	
Leu Arg Tyr Asp Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Thr Arg			
115	120	125	
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Pro Thr Pro Lys Ala Leu Lys Ala Gln Lys Thr Ala Ala Lys Thr Leu			
130	135	140	

Lys Ala Thr Ala Glu Thr Pro Phe Pro Val Thr Leu Gln Ser Ala Val
145 150 155 160

Ser Thr Thr Val Arg Arg Pro Lys Val Ser Arg Ser Gly Lys Glu Lys
165 170 175

Glu Glu Glu Glu Glu Val Leu Ile Val Glu Gly Ile Glu Phe Asp Arg
180 185 190

Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Glu
195 200 205

Gly Ile Thr Pro Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val
210 215 220

Pro His Lys His Lys His Ser Lys Lys Glu Lys Lys Leu Lys Thr Arg
225 230 235 240

Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp
245 250 255

Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys
260 265 270

Val Ser Val Ala Gly Leu Arg Ile Asp Phe Pro Asn
275 280

<210> 7
<211> 960
<212> DNA
<213> banana

<220>
<221> CDS
<222> (2).. (853)

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Leu Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asn Pro
1 5 10 15

ggc ggc gga tcc atc gag aac atg ccg cac aac aac gtc cac ttg tgg 97
Gly Ala Gly Ser Ile Glu Asn Met Pro His Asn Asn Val His Leu Trp
20 25 30

acc ggc gac cgc acc cag ccc aac ttc gag aac atg ggc acc ttc tac 145

Thr	Gly	Asp	Arg	Thr	Gln	Pro	Asn	Phe	Glu	Asn	Met	Gly	Thr	Phe	Tyr	
		35					40					45				
gcg	gcg	gcg	cgc	gac	ccc	atc	ttc	ttc	gcc	cac	cac	gcc	aac	atc	gac	193
Ala	Ala	Ala	Arg	Asp	Pro	Ile	Phe	Phe	Ala	His	His	Ala	Asn	Ile	Asp	
		50					55					60				
cga	atg	tgg	tac	ctg	tgg	aag	aag	ctc	agc	agg	aag	cac	cag	gac	ttc	241
Arg	Met	Trp	Tyr	Leu	Trp	Lys	Lys	Leu	Ser	Arg	Lys	His	Gln	Asp	Phe	
	65				70					75					80	
aat	gac	tgc	gac	tgg	ctc	aaa	gct	tcc	ttc	ctc	ttc	tac	gac	gag	aac	289
Asn	Asp	Ser	Asp	Trp	Leu	Lys	Ala	Ser	Phe	Leu	Phe	Tyr	Asp	Glu	Asn	
				85					90					95		
gcc	gac	tta	gtt	cgg	gtc	acg	gtc	aag	gac	tgc	ttg	gag	acc	gag	tgg	337
Ala	Asp	Leu	Val	Arg	Val	Thr	Val	Lys	Asp	Cys	Leu	Glu	Thr	Glu	Trp	
		100						105					110			
ctg	cgc	tac	acg	tac	caa	gac	gtg	aag	atc	cca	tgg	gcg	aac	acc	cga	385
Leu	Arg	Tyr	Thr	Tyr	Gln	Asp	Val	Lys	Ile	Pro	Trp	Ala	Asn	Thr	Arg	
		115					120						125			
ccg	act	ccc	aag	ctc	gcc	aag	gcg	agg	aaa	gcc	ggc	agc	aga	tgc	ctg	433
Pro	Thr	Pro	Lys	Leu	Ala	Lys	Ala	Arg	Lys	Ala	Gly	Ser	Arg	Ser	Leu	
		130				135					140					
aaa	gcc	acc	gcg	gag	gtg	cag	ttc	cct	gtg	acg	ctg	gaa	tcc	ccg	gtc	481
Lys	Ala	Thr	Ala	Glu	Val	Gln	Phe	Pro	Val	Thr	Leu	Glu	Ser	Pro	Val	
	145				150					155				160		
aaa	gtg	acg	gtg	aag	agg	ccc	aag	gtg	ggg	agg	agc	ggc	aag	gag	aag	529
Lys	Val	Thr	Val	Lys	Arg	Pro	Lys	Val	Gly	Arg	Ser	Gly	Lys	Glu	Lys	
				165				170					175			
gaa	gat	gag	gag	gag	ata	ctc	ata	gtg	gag	ggg	atc	gag	ttc	gac	cgc	577
Glu	Asp	Glu	Glu	Glu	Ile	Leu	Ile	Val	Glu	Gly	Ile	Glu	Phe	Asp	Arg	
		180						185					190			
gac	tac	ttc	atc	aag	ttc	gac	gtc	ttc	gtg	aac	gcg	acg	gag	ggc	gac	625
Asp	Tyr	Phe	Ile	Lys	Phe	Asp	Val	Phe	Val	Asn	Ala	Thr	Glu	Gly	Asp	
		195					200					205				
ggc	atc	acg	gcc	ggg	gcc	agt	gag	ttc	gcc	ggc	agc	ttc	gtg	aac	gtc	673
Gly	Ile	Thr	Ala	Gly	Ala	Ser	Glu	Phe	Ala	Gly	Ser	Phe	Val	Asn	Val	
		210					215					220				

ccg cac aag cac aag cac cgc aag gat gag aat aag ctg aag acg agg 721
 Pro His Lys His Lys His Arg Lys Asp Glu Asn Lys Leu Lys Thr Arg
 225 230 235 240

ctg tgt ctg gga atc acc gac ctg ctc gag gac atc ggc gcg gag gac 769
 Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp
 245 250 255

gac gac agc gtg ctc gtc acc atc gtg ccg aag gca ggc aaa gga aag 817
 Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys
 260 265 270

gtg tcc gtc ggc ggt ctt cgg att gac ttt tcc aag tgaggaaata 863
 Val Ser Val Gly Gly Leu Arg Ile Asp Phe Ser Lys
 275 280

aaagaattca cgtgccgtgc ctgctttcaa tgtacgaata aaataagagt gcatcatcac 923

cgaccatggt tctactttaaaaaa aaaaaaa 960

<210> 8
 <211> 284
 <212> PRT
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<400> 8
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Gly Ala Gly Ser Ile Glu Asn Met Pro His Asn Asn Val His Leu Trp
 20 25 30

Thr Gly Asp Arg Thr Gln Pro Asn Phe Glu Asn Met Gly Thr Phe Tyr
 35 40 45

Ala Ala Ala Arg Asp Pro Ile Phe Phe Ala His His Ala Asn Ile Asp
 50 55 60

Arg Met Trp Tyr Leu Trp Lys Lys Leu Ser Arg Lys His Gln Asp Phe
 65 70 75 80

Asn Asp Ser Asp Trp Leu Lys Ala Ser Phe Leu Phe Tyr Asp Glu Asn
 85 90 95

Ala Asp Leu Val Arg Val Thr Val Lys Asp Cys Leu Glu Thr Glu Trp
 100 105 110

Leu Arg Tyr Thr Tyr Gln Asp Val Lys Ile Pro Trp Ala Asn Thr Arg
115 120 125

Pro Thr Pro Lys Leu Ala Lys Ala Arg Lys Ala Gly Ser Arg Ser Leu
130 135 140

Lys Ala Thr Ala Glu Val Gln Phe Pro Val Thr Leu Glu Ser Pro Val
145 150 155 160

Lys Val Thr Val Lys Arg Pro Lys Val Gly Arg Ser Gly Lys Glu Lys
165 170 175

Glu Asp Glu Glu Glu Ile Leu Ile Val Glu Gly Ile Glu Phe Asp Arg
180 185 190

Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Asp
195 200 205

Gly Ile Thr Ala Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val
210 215 220

Pro His Lys His Lys His Arg Lys Asp Glu Asn Lys Leu Lys Thr Arg
225 230 235 240

Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp
245 250 255

Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys
260 265 270

Val Ser Val Gly Gly Leu Arg Ile Asp Phe Ser Lys
275 280

<210> 9

<211> 545

<212> DNA

<213> tobacco

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<221> CDS

<222> (1)..(543)

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1 5 10 15

atg cgt ttg cca cac atg ttt gat caa cca aac gtg tac cct gat ctt	96
Met Arg Leu Pro His Met Phe Asp Gln Pro Asn Val Tyr Pro Asp Leu	
20 25 30	
tac gat cca aga cgt aac caa gaa cac cgc ggt tct gta atc atg gac	144
Tyr Asp Pro Arg Arg Asn Gln Glu His Arg Gly Ser Val Ile Met Asp	
35 40 45	
ctt ggt cat ttt ggt caa gac gtg aaa gga act gac ttg caa atg atg	192
Leu Gly His Phe Gly Gln Asp Val Lys Gly Thr Asp Leu Gln Met Met	
50 55 60	
agc aat aac ctt act cta atg tat cgt caa atg att acc aat tca cca	240
Ser Asn Asn Leu Thr Leu Met Tyr Arg Gln Met Ile Thr Asn Ser Pro	
65 70 75 80	
tgt cca caa ctc ttt ttc ggt aag cca tat tgt acg gaa gtt gga ccc	288
Cys Pro Gln Leu Phe Phe Gly Lys Pro Tyr Cys Thr Glu Val Gly Pro	
85 90 95	
aaa cca ggg cag gga gct att gaa aac atc cct cat act cct gtc cac	336
Lys Pro Gly Gln Gly Ala Ile Glu Asn Ile Pro His Thr Pro Val His	
100 105 110	
att tgg gtt ggt agt aag cct aat gag aat aac tgt aaa aac ggt gaa	384
Ile Trp Val Gly Ser Lys Pro Asn Glu Asn Asn Cys Lys Asn Gly Glu	
115 120 125	
gat atg gga aat ttc tat tca gct ggt aag gat cct gct ttc tat agt	432
Asp Met Gly Asn Phe Tyr Ser Ala Gly Lys Asp Pro Ala Phe Tyr Ser	
130 135 140	
cac cat gca aat gta gat cgc atg tgg aca ata tgg aaa aca tta gga	480
His His Ala Asn Val Asp Arg Met Trp Thr Ile Trp Lys Thr Leu Gly	
145 150 155 160	
gga aaa cgc aag gac atc aac aag cca gat tat ttg aac act gag ttc	528
Gly Lys Arg Lys Asp Ile Asn Lys Pro Asp Tyr Leu Asn Thr Glu Phe	
165 170 175	
ttt ttc tac gac gaa aa	545
Phe Phe Tyr Asp Glu	
180	

<210> 10

<211> 181

<212> PRT

<213> tobacco

<400> 10

Asp Pro Thr Phe Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly
1 5 10 15

Met Arg Leu Pro His Met Phe Asp Gln Pro Asn Val Tyr Pro Asp Leu
20 25 30

Tyr Asp Pro Arg Arg Asn Gln Glu His Arg Gly Ser Val Ile Met Asp
35 40 45

Leu Gly His Phe Gly Gln Asp Val Lys Gly Thr Asp Leu Gln Met Met
50 55 60

Ser Asn Asn Leu Thr Leu Met Tyr Arg Gln Met Ile Thr Asn Ser Pro
65 70 75 80

Cys Pro Gln Leu Phe Phe Gly Lys Pro Tyr Cys Thr Glu Val Gly Pro
85 90 95

Lys Pro Gly Gln Gly Ala Ile Glu Asn Ile Pro His Thr Pro Val His
100 105 110

Ile Trp Val Gly Ser Lys Pro Asn Glu Asn Asn Cys Lys Asn Gly Glu
115 120 125

Asp Met Gly Asn Phe Tyr Ser Ala Gly Lys Asp Pro Ala Phe Tyr Ser
130 135 140

His His Ala Asn Val Asp Arg Met Trp Thr Ile Trp Lys Thr Leu Gly
145 150 155 160

Gly Lys Arg Lys Asp Ile Asn Lys Pro Asp Tyr Leu Asn Thr Glu Phe
165 170 175

Phe Phe Tyr Asp Glu
180

<210> 11

<211> 673

<212> DNA

<213> tobacco

<220>

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<222> (3)..(671)

<400> 11

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1 5 10 15	
tta caa gtc cat ttc tcg tgg ctt ttt ttc cct ttt cat aga tgg tac	95
Leu Gln Val His Phe Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr	
20 25 30	
ttg tac ttc tat gaa aga atc ttg ggc tct tta att aat gat cct act	143
Leu Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr	
35 40 45	
ttt ggt ttg cca tat tgg aac tgg gac cat cca aag ggc atg cgt ata	191
Phe Gly Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly Met Arg Ile	
50 55 60	
cct ccc atg ttc gat cgt gaa ggg tct tcc ctt tac gac gaa aaa cgt	239
Pro Pro Met Phe Asp Arg Glu Gly Ser Ser Leu Tyr Asp Glu Lys Arg	
65 70 75	
aac caa agt cac cgt aat gga acc ata att gat ctt ggt cat ttc ggt	287
Asn Gln Ser His Arg Asn Gly Thr Ile Ile Asp Leu Gly His Phe Gly	
80 85 90 95	
caa gaa gtc caa aca act caa ctg cag cag atg act aat aac tta act	335
Gln Glu Val Gln Thr Thr Gln Leu Gln Gln Met Thr Asn Asn Leu Thr	
100 105 110	
ata atg tat cgt caa atg ata act aat gct cct tgc ccc ttg ctc ttc	383
Ile Met Tyr Arg Gln Met Ile Thr Asn Ala Pro Cys Pro Leu Leu Phe	
115 120 125	
ttt ggt cag cct tac cct cta gga act gat ccc agt cca ggg atg ggc	431
Phe Gly Gln Pro Tyr Pro Leu Gly Thr Asp Pro Ser Pro Gly Met Gly	
130 135 140	
act att gaa aac atc cct cat act cct gtc cac att tgg gtt ggt agt	479
Thr Ile Glu Asn Ile Pro His Thr Pro Val His Ile Trp Val Gly Ser	
145 150 155	
agg ctt gat gag aat aat acg aaa cac ggt gag gat atg ggt aat ttt	527
Arg Leu Asp Glu Asn Asn Thr Lys His Gly Glu Asp Met Gly Asn Phe	
160 165 170 175	

tac tgc gcc ggt tta gac ccg ctt ttc tat tcc cat cac gcc aat gtg 575
Tyr Ser Ala Gly Leu Asp Pro Leu Phe Tyr Ser His His Ala Asn Val
180 185 190

gac cgg atg tgg tcc gag tgg aaa gcc tta gga ggg aaa aga agg gat 623
Asp Arg Met Trp Ser Glu Trp Lys Ala Leu Gly Gly Lys Arg Arg Asp
195 200 205

ctc acg cac aaa gat tgg ttg aac tcc gag ttc ttt ttc tac gat gaa 671
Leu Thr His Lys Asp Trp Leu Asn Ser Glu Phe Phe Phe Tyr Asp Glu
210 215 220

aa 673

<210> 12
<211> 223
<212> PRT
<213> tobacco

<400> 12
His Cys Ala Tyr Cys Asn Gly Ala Tyr Lys Ile Gly Gly Lys Glu Leu
1 5 10 15

Gln Val His Phe Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr Leu
20 25 30

Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr Phe
35 40 45

Gly Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly Met Arg Ile Pro
50 55 60

Pro Met Phe Asp Arg Glu Gly Ser Ser Leu Tyr Asp Glu Lys Arg Asn
65 70 75 80

Gln Ser His Arg Asn Gly Thr Ile Ile Asp Leu Gly His Phe Gly Gln
85 90 95

Glu Val Gln Thr Thr Gln Leu Gln Gln Met Thr Asn Asn Leu Thr Ile
100 105 110

Met Tyr Arg Gln Met Ile Thr Asn Ala Pro Cys Pro Leu Leu Phe Phe
115 120 125

Gly Gln Pro Tyr Pro Leu Gly Thr Asp Pro Ser Pro Gly Met Gly Thr
130 135 140

Ile Glu Asn Ile Pro His Thr Pro Val His Ile Trp Val Gly Ser Arg
145 150 155 160

Leu Asp Glu Asn Asn Thr Lys His Gly Glu Asp Met Gly Asn Phe Tyr
165 170 175

Ser Ala Gly Leu Asp Pro Leu Phe Tyr Ser His His Ala Asn Val Asp
180 185 190

Arg Met Trp Ser Glu Trp Lys Ala Leu Gly Gly Lys Arg Arg Asp Leu
195 200 205

Thr His Lys Asp Trp Leu Asn Ser Glu Phe Phe Phe Tyr Asp Glu
210 215 220

<210> 13

<211> 685

<212> DNA

<213> tobacco

<220>

<221> CDS

<222> (3)..(683)

<400> 13

tg cat tgt gcg tat tgc aac gat gct tac aca atg ggt gac caa aag 47
His Cys Ala Tyr Cys Asn Asp Ala Tyr Thr Met Gly Asp Gln Lys
1 5 10 15

tta caa gtt cac caa tcg tgg ctt ttc ttc ccg ttt cat aga tgg tac 95
Leu Gln Val His Gln Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr
20 25 30

ttg tac ttc tac gag aga atc ttg ggc tcc ctc atc gat gat cca act 143
Leu Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asp Asp Pro Thr
35 40 45

ttt gct ctg cca tat tgg aac tgg gac cat cca agc ggc atg cgt ttg 191
Phe Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Ser Gly Met Arg Leu
50 55 60

cct gct atg ttc gat gtc gaa ggt tct tcc ctc tac gat gca aga cgt 239
~~Pro Ala Met Phe Asp Val Glu Gly Ser Ser Leu Tyr Asp Ala Arg Arg~~
65 70 75

aat cca cat gtc cgt aat gga acc ata atc gat ctt ggt ttt ttc ggt 287

[illegible]

<210> 14
<211> 227
<212> PRT
<213> tobacco

<400> 14
His Cys Ala Tyr Cys Asn Asp Ala Tyr Thr Met Gly Asp Gln Lys Leu

1	5	10	15
Gln Val His Gln Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr Leu	20	25	30
Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asp Asp Pro Thr Phe	35	40	45
Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Ser Gly Met Arg Leu Pro	50	55	60
Ala Met Phe Asp Val Glu Gly Ser Ser Leu Tyr Asp Ala Arg Arg Asn	65	70	75 80
Pro His Val Arg Asn Gly Thr Ile Ile Asp Leu Gly Phe Phe Gly Asp	85	90	95
Glu Val Lys Thr Asn Glu Ile Gln Met Ile Thr Asn Asn Leu Ile Leu	100	105	110
Met Tyr Arg Gln Met Ile Thr Asn Ala Pro Cys Pro Leu Leu Phe Phe	115	120	125
Gly Glu Pro Tyr Arg Phe Gly Ser Lys Pro Asn Pro Gly Gln Gly Thr	130	135	140
Ile Glu Asn Ile Pro His Thr Pro Val His Ile Trp Thr Gly Thr Val	145	150	155 160
Arg Cys Thr Asp Leu Gly Asn Cys Val Pro Ser Tyr Gly Glu Asp Met	165	170	175
Gly Asn Phe Tyr Ser Ala Gly Leu Asp Pro Val Phe Tyr Ser His His	180	185	190
Ala Asn Val Asp Arg Met Trp Asn Glu Trp Lys Ala Leu Gly Gly Lys	195	200	205
Arg Arg Asp Leu Thr Asp Asn Asp Trp Leu Asn Ser Glu Phe Phe Phe	210	215	220
Tyr Asp Glu	225		

<210> 15

<211> 670

<212> DNA

<213> pineapple

<220>

<221> CDS

<222> (3)..(668)

<400> 15

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His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro	
1 5 10 15	
gat ctc gag atc cag atc cac aac tgc tgg ctc ttc ttt cct tgg cac	95
Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His	
20 25 30	
cgg ttc tac ctc tac ttc aac gag cgc ata ctc ggg aaa ctt atc ggc	143
Arg Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly	
35 40 45	
gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg ccg ggg ggc	191
Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly	
50 55 60	
atg cag ttc ccg tct atc tac acg gac cct tca tcc tgc cta tat gac	239
Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp	
65 70 75	
aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att gac ctc gac	287
Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp	
80 85 90 95	
tac aat ggc acc gat cct acc ttc tcc cct gaa gaa cag att aac cac	335
Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His	
100 105 110	
aac ctc gcc gtc atg tac cga cag gtg ata tcc agt gga aag aca cca	383
Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro	
115 120 125	
gag ctg ttt atg ggc tca gcg tac cgc gcc ggt gac cag cct gac ccc	431
Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro	
130 135 140	
ggc gca ggt tct gta gag cag aag ccg cac gcc ccg gtg cat gtg tgg	479
Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp	
145 150 155	

aca ggt gat cgc aac cag ccc aat cgc gaa gac atg ggc acg ctc tac 527
 Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr
 160 165 170 175

tcg gcg gcg tgg gac ccc gtt ttt ttc gca cac cac ggc aac atc gac 575
 Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp
 180 185 190

cgc atg tgg tac gtg tgg agg aac ctt ggc ggc aag cac cgc aac ttc 623
 Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe
 195 200 205

acc gac ccc gac tgg ctc aac gcg tcc ttc ctg ttc tac gac gaa aa 670
 Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu
 210 215 220

<210> 16
 <211> 222
 <212> PRT
 <213> pineapple

<400> 16
 His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asp
 1 5 10 15

Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His Arg
 20 25 30

Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp
 35 40 45

Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met
 50 55 60

Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp Lys
 65 70 75 80

Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp Tyr
 85 90 95

Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His Asn
 100 105 110

Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro Glu
 115 120 125

Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro Gly

130	135	140
Ala Gly Ser Val Glu Gln Lys Pro His Gly Pr Val His Val Trp Thr		
145	150	155 160
Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr Ser		
165	170	175
Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp Arg		
180	185	190
Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe Thr		
195	200	205
Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu		
210	215	220

<210> 17
 <211> 1319
 <212> DNA
 <213> pineapple

 <220>
 <221> CDS
 <222> (1)..(1053)

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Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Gln Ile Pro Ala	
1 5 10 15	
atc tac gcc gac gct tcg tcc ccg ctc tac gac aag ctg cgc aat gcg	96
Ile Tyr Ala Asp Ala Ser Ser Pro Leu Tyr Asp Lys Leu Arg Asn Ala	
20 25 30	
aag cac cag ccg ccg act ttg gtc gac ctc gac tac aac ggc acc gac	144
Lys His Gln Pro Pro Thr Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp	
35 40 45	
ccg acc ttc acc cct gag cag cag atc gcc cac aac ctc acc atc atg	192
Pro Thr Phe Thr Pro Glu Gln Gln Ile Ala His Asn Leu Thr Ile Met	
50 55 60	

tac cga cag gtg ata tcc ggc ggg aag acg ccg gag ttg ttt atg ggc	240
Tyr Arg Gln Val Ile Ser Gly Gly Lys Thr Pro Glu Leu Phe Met Gly	
65 70 75 80	

gcg gcg tac cgc gcg ggc gac gcg cca gac ccg ggc gca ggc act cta	288
Ala Ala Tyr Arg Ala Gly Asp Ala Pro Asp Pro Gly Ala Gly Thr Leu	
85 90 95	
gag ctc gtg ccg cac aac acg atg cat ttg tgg acc ggc gac ccc aac	336
Glu Leu Val Pro His Asn Thr Met His Leu Trp Thr Gly Asp Pro Asn	
100 105 110	
caa ccc aac gac gaa gac atg ggc acg ttc tac gcg gcg gcg cgg gac	384
Gln Pro Asn Asp Glu Asp Met Gly Thr Phe Tyr Ala Ala Ala Arg Asp	
115 120 125	
ccc atc ttc ttc gcc cac cac ggc aac gtc gac cgc atg tgg tac gtg	432
Pro Ile Phe Phe Ala His His Gly Asn Val Asp Arg Met Trp Tyr Val	
130 135 140	
tgg cgg aaa ctc ggg ggc acg cac cgc gat ttc acc gac ccc gac tgg	480
Trp Arg Lys Leu Gly Gly Thr His Arg Asp Phe Thr Asp Pro Asp Trp	
145 150 155 160	
ctc aac gcg tcc ttc ctc ttc tac gac gag aac gcg cag ctc gtc cgc	528
Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn Ala Gln Leu Val Arg	
165 170 175	
gtc aaa gta aag gac tgc ttg agc gcc gac gcg ctg cgg tac acg tac	576
Val Lys Val Lys Asp Cys Leu Ser Ala Asp Ala Leu Arg Tyr Thr Tyr	
180 185 190	
cag gac gtc gac atc ccg tgg atc agt gcg aag ccg acg ccg aag aaa	624
Gln Asp Val Asp Ile Pro Trp Ile Ser Ala Lys Pro Thr Pro Lys Lys	
195 200 205	
aca ccg ggg ggc gct gcg cct tcc acg aca gag gct ata ttt ccg gtg	672
Thr Pro Gly Gly Ala Ala Pro Ser Thr Thr Glu Ala Ile Phe Pro Val	
210 215 220	
gtg ctg gat aag ccg gtg agc tct acg gtg gcg agg ccg aag acg ggg	720
Val Leu Asp Lys Pro Val Ser Ser Thr Val Ala Arg Pro Lys Thr Gly	
225 230 235 240	
agg agt act ggg gag gag gag gtg ttg gtg gtg gag gga atc gag ctg	768
Arg Ser Thr Gly Glu Glu Glu Val Leu Val Val Glu Gly Ile Glu Leu	
245 250 255	
gac aag gac gtg gcc gtg aag ttc gac gtg tat ata aac gcg ccg gac	816
Asp Lys Asp Val Ala Val Lys Phe Asp Val Tyr Ile Asn Ala Pro Asp	
260 265 270	

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aac gaa ggg gtg ggg ccg gag gcg agc gag ttc gca ggg agc ttc gtc 864
Asn Glu Gly Val Gly Pro Glu Ala Ser Glu Phe Ala Gly Ser Phe Val
      275              280              285

cag gtg ccg cac aag cac aag aag ggg aag aag gag aag gcg agg att 912
Gln Val Pro His Lys His Lys Lys Gly Lys Lys Glu Lys Ala Arg Ile
      290              295              300

aaa acg acg ctc agg ctc ggg ata acg gac ctg ctc gag gac atc ggc 960
Lys Thr Thr Leu Arg Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly
      305              310              315              320

gcc gag gac gac gag agc gtg ctc gtc acg ctc gtg ccg agg ata ggc 1008
Ala Glu Asp Asp Glu Ser Val Leu Val Thr Leu Val Pro Arg Ile Gly
              325              330              335

gag ggg ttg gtc aag gtt ggt ggg cta agg atc gat ttc tcc aag 1053
Glu Gly Leu Val Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys
      340              345              350

tgatcagcag caaattaact atacatgaaa gtaaaaaaaaa ttgcatttac ctacctatag 1113

aagagaataa atgcgtatgt aatctgcccc atttgtcact ttttaatttct cgagcgtgtt 1173

ctgaatgaga gttgcatgca tgcgcgcagc cataatgcct ggtatagtgt agtagtttag 1233

gcgtggatgc gtataacgta cgtatgcatg tataaggaat aatgatgagt ttactatgca 1293

aaaaaaaaaa aaaaaaaaaa aaaaaa 1319

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<212> PRT
<213> pineapple

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Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Gln Ile Pro Ala
  1              5              10              15

Ile Tyr Ala Asp Ala Ser Ser Pro Leu Tyr Asp Lys Leu Arg Asn Ala
      20              25              30

Lys His Gln Pro Pro Thr Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp
      35              40              45

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Pro Thr Phe Thr Pro Glu Gln Gln Ile Ala His Asn Leu Thr Ile Met
50 55 60

Tyr Arg Gln Val Ile Ser Gly Gly Lys Thr Pro Glu Leu Phe Met Gly
65 70 75 80

Ala Ala Tyr Arg Ala Gly Asp Ala Pro Asp Pro Gly Ala Gly Thr Leu
85 90 95

Glu Leu Val Pro His Asn Thr Met His Leu Trp Thr Gly Asp Pro Asn
100 105 110

Gln Pro Asn Asp Glu Asp Met Gly Thr Phe Tyr Ala Ala Ala Arg Asp
115 120 125

Pro Ile Phe Phe Ala His His Gly Asn Val Asp Arg Met Trp Tyr Val
130 135 140

Trp Arg Lys Leu Gly Gly Thr His Arg Asp Phe Thr Asp Pro Asp Trp
145 150 155 160

Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn Ala Gln Leu Val Arg
165 170 175

Val Lys Val Lys Asp Cys Leu Ser Ala Asp Ala Leu Arg Tyr Thr Tyr
180 185 190

Gln Asp Val Asp Ile Pro Trp Ile Ser Ala Lys Pro Thr Pro Lys Lys
195 200 205

Thr Pro Gly Gly Ala Ala Pro Ser Thr Thr Glu Ala Ile Phe Pro Val
210 215 220

Val Leu Asp Lys Pro Val Ser Ser Thr Val Ala Arg Pro Lys Thr Gly
225 230 235 240

Arg Ser Thr Gly Glu Glu Glu Val Leu Val Val Glu Gly Ile Glu Leu
245 250 255

Asp Lys Asp Val Ala Val Lys Phe Asp Val Tyr Ile Asn Ala Pro Asp
260 265 270

Asn Glu Gly Val Gly Pro Glu Ala Ser Glu Phe Ala Gly Ser Phe Val
275 280 285

Gln Val Pro His Lys His Lys Lys Gly Lys Lys Glu Lys Ala Arg Ile
290 295 300

Lys Thr Thr Leu Arg Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly
305 310 315 320

Ala Glu Asp Asp Glu Ser Val Leu Val Thr Leu Val Pro Arg Ile Gly
325 330 335

Glu Gly Leu Val Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys
340 345 350

<210> 19

<211> 2181

<212> DNA

<213> pineapple

<220>

<221> CDS

<222> (2)..(1858)

<400> 19

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Gly Ile Asp Lys Leu Asp Pro Val Pro Gly Leu Gly Val Phe Thr Met

1 5 10 15

gcc acc ctc tct aaa cta gct tcc caa cca ata aca cct cca ctc tcc 97

Ala Thr Leu Ser Lys Leu Ala Ser Gln Pro Ile Thr Pro Pro Leu Ser

20 25 30

ccg ctc cct cct ttg cat gct cct tct ctc acc aaa agc ttc acc acc 145

Pro Leu Pro Pro Leu His Ala Pro Ser Leu Thr Lys Ser Phe Thr Thr

35 40 45

acc ttc ctc tcc cct gta ggg gtc cca aac cac ccc gtc ata aga tct 193

Thr Phe Leu Ser Pro Val Gly Val Pro Asn His Pro Val Ile Arg Ser

50 55 60

cat gca aat cta agg agc aac aag aga atg ccg aca agc ctg cgg gcc 241

His Ala Asn Leu Arg Ser Asn Lys Arg Met Pro Thr Ser Leu Arg Ala

65 70 75 80

gca tcg ccc gcc gcg acc tac tcc tgg gcc ctc ggc ggg ctt tac ggt 289

Ala Ser Pro Ala Ala Thr Tyr Ser Trp Ala Leu Gly Gly Leu Tyr Gly

85 90 95

gcc acc act ggg ctc ggc ctc aac cgt cga gcg gcc gcc gcc cct atc 337

Ala Thr Thr Gly Leu Gly Leu Asn Arg Arg Ala Ala Ala Ala Pro Ile

100 105 110

ctg gct ccc gac ctc tca act tgt ggg ccg cct gcc gac ctc cct gcc	385
Leu Ala Pro Asp Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala	
115 120 125	
tcc gcc cga ccg aca gtt tgc tgc ccg cca tac caa tcc acc atc atc	433
Ser Ala Arg Pro Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile	
130 135 140	
gac ttc aag ctc ccc ccg cga tct gct ccg ctt cgc gtc ccg cct gcg	481
Asp Phe Lys Leu Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala	
145 150 155 160	
gcc cac ttg gtt gac gcc gac tac ctg gcc aag tat aag aag gcg gtc	529
Ala His Leu Val Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val	
165 170 175	
gag ctc atg agg gcc ctg ccg gcc gac gac ccg cgc aac ttc gta cag	577
Glu Leu Met Arg Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln	
180 185 190	
caa gcg aaa gtg cac tgt gcg tat tgc gac ggc gcg tat gac caa atc	625
Gln Ala Lys Val His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile	
195 200 205	
ggc ttc ccc gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt	673
Gly Phe Pro Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe	
210 215 220	
cct tgg cac ccg ttc tac ctc tac tcc aac gag cgc ata ctc ggg aaa	721
Pro Trp His Arg Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys	
225 230 235 240	
ctt atc ggc gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg	769
Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala	
245 250 255	
ccg ggg ggc atg cag ttc ccg tct atc tac aca gac cct tca tcc tcg	817
Pro Gly Gly Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser	
260 265 270	
cta tat gac aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att	865
Leu Tyr Asp Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile	
275 280 285	

gac ctc gac tac aat ggc acc gat cct acc ttc tcc cct gaa gaa cag	913
Asp Leu Asp Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln	
290 295 300	

att aac cac aac ctc gcc gtc atg tac cga cag gtg ata tcc agt gga	961
Ile Asn His Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly	
305 310 315 320	
aag acg cca gag ctg ttt atg ggc tca gcg tac cgc gcc ggt gac cag	1009
Lys Thr Pro Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln	
325 330 335	
cct gac ccc ggc gca ggc tct gta gag cag aag ccg cac ggc ccg gtg	1057
Pro Asp Pro Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val	
340 345 350	
cat gtg tgg aca ggt gat cgc aac cag ccc aat cgc gaa gac atg ggc	1103
His Val Trp Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly	
355 360 365	
acg ctc tac tcg gcg gcg tgg gac ccc gtc ttc ttc gca cac cac ggc	1153
Thr Leu Tyr Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly	
370 375 380	
aac atc gac cgc atg tgg tac gtg tgg agg aac ctt ggc ggc aag cac	1201
Asn Ile Asp Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His	
385 390 395 400	
cgc aac ttc acc gac ccc gac tgg ctc aac gcg tcc ttc ctg ttc tat	1249
Arg Asn Phe Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr	
405 410 415	
gat gag aat gcg cag ctc gtc cgt gtt aaa gta aaa gac tgc tta gag	1297
Asp Glu Asn Ala Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu	
420 425 430	
gcc gac gca atg cgg tac aca tac cag gat gta gag atc ccg tgg ctc	1345
Ala Asp Ala Met Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu	
435 440 445	
aaa gca aag ccg acg cca aag agc gcc cta cag aag ata aag agc aag	1393
Lys Ala Lys Pro Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys	
450 455 460	
gta tcg acg ctg aag gca aca cca agg ggg acg acg act acc aca gca	1441
Val Ser Thr Leu Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Ala	
465 470 475 480	
gag act acatttt ccg gtg gtg ctg gat aag ccg gtg agt gca aca gtg	1485
Glu Thr Thr Thr Phe Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val	

485	490	495	
gct aga ccg aag gcc agg agg agt ggg aag gag aag gaa gaa gag gag			1537
Ala Arg Pro Lys Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu			
500	505	510	
gag gtg ttg gtg gtg gag gga atc gag ttg gag aag gac gtg ttc gtg			1585
Glu Val Leu Val Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val			
515	520	525	
aag ttt gat gtg tat ata aac tcg ccg gag cac gaa ggg gtg ggg ccg			1633
Lys Phe Asp Val Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro			
530	535	540	
gag gcg agt gag ttc gca ggg agc ttc gtc cac gtg cca cac aag cac			1681
Glu Ala Ser Glu Phe Ala Gly Ser Phe Val His Val Pro His Lys His			
545	550	555	560
aag aag gcg aag aag ggg aag gag atg gcc agg atg aac aca agg ctt			1729
Lys Lys Ala Lys Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu			
565	570	575	
aag ctc ggg ata acg gac ctg ctc gag gac atc ggc gct gag gac gac			1777
Lys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp			
580	585	590	
gag agc gtg ctc atc acg ctc gtg ccc agg agc ggc aag gga atg gtg			1825
Glu Ser Val Leu Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val			
595	600	605	
aag gtt gga ggg cta agg att gat ttc tcc aag tgatgagcat attgtgaaga			1878
Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys			
610	615		
gaaaaatttc atttaccgcc ctatagaatc gaaaaatttc gtatatgtcc cattattgtt 1938			
ttttttattc ttcaagcgta ttcagaataa gagttgcgtg catgcacgca tgcagccatg 1998			
ttgttgtagt cgatatgtgg ggtatgtttg gatcagggat aatgatgtga actttgaatt 2058			
aattattaca ctctgagaat aaattagaga gtttattatg caagttgctt ggtgtaatatg 2118			
atattcaaca ttgtttccta tacatctttt ttggaagaa aaaaaaaaaa aaaaaaaatc 2178			
gat			2181

<211> 619
 <212> PRT
 <213> pineapple

<400> 20

Gly Ile Asp Lys Leu Asp Pro Val Pro Gly Leu Gly Val Phe Thr Met
 1 5 10 15

Ala Thr Leu Ser Lys Leu Ala Ser Gln Pro Ile Thr Pro Pro Leu Ser
 20 25 30

Pro Leu Pro Pro Leu His Ala Pro Ser Leu Thr Lys Ser Phe Thr Thr
 35 40 45

Thr Phe Leu Ser Pro Val Gly Val Pro Asn His Pro Val Ile Arg Ser
 50 55 60

His Ala Asn Leu Arg Ser Asn Lys Arg Met Pro Thr Ser Leu Arg Ala
 65 70 75 80

Ala Ser Pro Ala Ala Thr Tyr Ser Trp Ala Leu Gly Gly Leu Tyr Gly
 85 90 95

Ala Thr Thr Gly Leu Gly Leu Asn Arg Arg Ala Ala Ala Ala Pro Ile
 100 105 110

Leu Ala Pro Asp Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala
 115 120 125

Ser Ala Arg Pro Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile
 130 135 140

Asp Phe Lys Leu Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala
 145 150 155 160

Ala His Leu Val Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val
 165 170 175

Glu Leu Met Arg Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln
 180 185 190

Gln Ala Lys Val His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile
 195 200 205

Gly Phe Pro Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe
 210 215 220

Pro Trp His Arg Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys
225 230 235 240

Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala
245 250 255

Pro Gly Gly Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser
260 265 270

Leu Tyr Asp Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile
275 280 285

Asp Leu Asp Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln
290 295 300

Ile Asn His Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly
305 310 315 320

Lys Thr Pro Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln
325 330 335

Pro Asp Pro Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val
340 345 350

His Val Trp Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly
355 360 365

Thr Leu Tyr Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly
370 375 380

Asn Ile Asp Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His
385 390 395 400

Arg Asn Phe Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr
405 410 415

Asp Glu Asn Ala Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu
420 425 430

Ala Asp Ala Met Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu
435 440 445

Lys Ala Lys Pro Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys
450 455 460

Val Ser Thr Leu Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Ala
465 470 475 480

Glu Thr Thr Phe Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val
485 490 495

Ala Arg Pro Lys Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu Glu
500 505 510

Glu Val Leu Val Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val
515 520 525

Lys Phe Asp Val Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro
530 535 540

Glu Ala Ser Glu Phe Ala Gly Ser Phe Val His Val Pro His Lys His
545 550 555 560

Lys Lys Ala Lys Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu
565 570 575

Lys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp
580 585 590

Glu Ser Val Leu Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val
595 600 605

Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys
610 615

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<211> 2078

<212> DNA

<213> banana

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<222> (53)..(1822)

<400> 21

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Met Ser
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Leu Leu Leu Asn Ser Ser Phe Thr Gly Ala Ser Ser Ala Cys Leu Leu
5 10 15

caa cgg gaa agg tcc cgc cgc cgc cgc ctc cac gtc cct ggc gtg aca 154
Gln Arg Glu Arg Ser Arg Arg Arg Arg Leu His Val Pro Gly Val Thr
20 25 30

tgc cgc cag ggc agt aat ggt gac cgc aga gat gcc gcc ccc cag cag 202
Cys Arg Gln Gly Ser Asn Gly Asp Arg Arg Asp Ala Ala Pro Gln Gln
35 40 45 50

cag tcg ccg ccg ctg ctg gat cgg cgc gac atg ctg ttg ggt tta gga 250
Gln Ser Pro Pro Leu Leu Asp Arg Arg Asp Met Leu Leu Gly Leu Gly
55 60 65

ggg ctt tac ggc gtg acc gca gga ccc aag gtt ctg gcg gcg ccg ata 298
Gly Leu Tyr Gly Val Thr Ala Gly Pro Lys Val Leu Ala Ala Pro Ile
70 75 80

atg ccg ccg gat ctg tcc aag tgc tac cct gcc acc gca cct gcc ctc 346
Met Pro Pro Asp Leu Ser Lys Cys Tyr Pro Ala Thr Ala Pro Ala Leu
85 90 95

gac aac aaa tgc tgc ccg cct tac gac ccc ggc gag acg atc tcg gag 394
Asp Asn Lys Cys Cys Pro Pro Tyr Asp Pro Gly Glu Thr Ile Ser Glu
100 105 110

tac agc ttc cct gct acg ccc ctc cgg gtg cgg cgg ccg gcc cat atc 442
Tyr Ser Phe Pro Ala Thr Pro Leu Arg Val Arg Arg Pro Ala His Ile
115 120 125 130

gtg aag gac gat cag gag tat atg gac aag tac aag gag gca gtg agg 490
Val Lys Asp Asp Gln Glu Tyr Met Asp Lys Tyr Lys Glu Ala Val Arg
135 140 145

agg atg aag aat ctg ccg gca gac cac cct tgg aac tac tac cag cag 538
Arg Met Lys Asn Leu Pro Ala Asp His Pro Trp Asn Tyr Tyr Gln Gln
150 155 160

gcg aac atc cac tgc cag tat tgc aac tac gcc tac cac cag caa aat 586
Ala Asn Ile His Cys Gln Tyr Cys Asn Tyr Ala Tyr His Gln Gln Asn
165 170 175

acc gac gac gtg ccc atc cag gtc cac ttc agc tgg atc ttc ctc cca 634
Thr Asp Asp Val Pro Ile Gln Val His Phe Ser Trp Ile Phe Leu Pro
180 185 190

tgg cac cgc tac tac ctc cac ttc tac gaa agg atc ctc ggc aag ctc 682
Trp His Arg Tyr Tyr Leu His Phe Tyr Glu Arg Ile Leu Gly Lys Leu
195 200 205 210

atc gac gac gac acc ttc acc atc cca ttc tgg aac tgg gac acc aag	730
Ile Asp Asp Asp Thr Phe Thr Ile Pro Phe Trp Asn Trp Asp Thr Lys	
215 220 225	
gac ggg atg acg ttc ccc gcc atc ttc cag gat gcg gca tcc ccg ctg	778
Asp Gly Met Thr Phe Pro Ala Ile Phe Gln Asp Ala Ala Ser Pro Leu	
230 235 240	
tac gac ccg aga cgc gac caa cgc cac gtc aag gac ggc aag atc ctc	826
Tyr Asp Pro Arg Arg Asp Gln Arg His Val Lys Asp Gly Lys Ile Leu	
245 250 255	
gac ctc aag tac gcc tac acc gaa aac act gca tcc gac agc gag atc	874
Asp Leu Lys Tyr Ala Tyr Thr Glu Asn Thr Ala Ser Asp Ser Glu Ile	
260 265 270	
ata cgg gag aac ctc tgc ttc ata cag aag acg ttc aag cac agc ctg	922
Ile Arg Glu Asn Leu Cys Phe Ile Gln Lys Thr Phe Lys His Ser Leu	
275 280 285 290	
tcg ctg gcg gaa ctg ttc atg ggg gat ccc gtg cgc gcg ggg gag aag	970
Ser Leu Ala Glu Leu Phe Met Gly Asp Pro Val Arg Ala Gly Glu Lys	
295 300 305	
gag atc cag gag gct aat ggg cag atg gaa gtc atc cac aat gcg gcg	1018
Glu Ile Gln Glu Ala Asn Gly Gln Met Glu Val Ile His Asn Ala Ala	
310 315 320	
cac atg tgg gtc gga gag ccg gac gga tac aag gaa aac atg ggg gac	1066
His Met Trp Val Gly Glu Pro Asp Gly Tyr Lys Glu Asn Met Gly Asp	
325 330 335	
ttc tcc acc gcc gcc cgc gat tct gtt ttc ttc tgc cac cat tcc aat	1114
Phe Ser Thr Ala Ala Arg Asp Ser Val Phe Phe Cys His His Ser Asn	
340 345 350	
gtc gac cgc atg tgg gac atc tac cgc aac ctc cgc ggc aac cgc gtc	1162
Val Asp Arg Met Trp Asp Ile Tyr Arg Asn Leu Arg Gly Asn Arg Val	
355 360 365 370	
gag ttc gaa gac aac gac tgg ttg gac agc acc ttc ctc ttc cac gac	1210
Glu Phe Glu Asp Asn Asp Trp Leu Asp Ser Thr Phe Leu Phe His Asp	
375 380 385	
gag aac gaa cag ctc gtc aaa gtc aag atg agc gac tgc ctc aac ccg	1258
Glu Asn Glu Gln Leu Val Lys Val Lys Met Ser Asp Cys Leu Asn Pro	
390 395 400	

acc aag ctt cgg tac acg ttc gag caa gtt ccc ctc cca tgg ctg ggc	1306
Thr Lys Leu Arg Tyr Thr Phe Glu Gln Val Pro Leu Pro Trp Leu Gly	
405 410 415	
aaa atc aat tgc cag aag acg gca gag acg aag tcc aag gcc acg acg	1354
Lys Ile Asn Cys Gln Lys Thr Ala Glu Thr Lys Ser Lys Ala Thr Thr	
420 425 430	
gag ctg tcg ctg acg cgc gtg aac gaa ttc ggg acg acg gcc cag gca	1402
Glu Leu Ser Leu Thr Arg Val Asn Glu Phe Gly Thr Thr Ala Gln Ala	
435 440 445 450	
ctc gac gcg agc aac ccg ctg cgg gtg atc gtg gca agg ccg aag aag	1450
Leu Asp Ala Ser Asn Pro Leu Arg Val Ile Val Ala Arg Pro Lys Lys	
455 460 465	
aac cgc aag aag aag gag aag caa gag aag gtg ggg gtg att cag atc	1498
Asn Arg Lys Lys Lys Glu Lys Gln Glu Lys Val Gly Val Ile Gln Ile	
470 475 480	
aag gat att aag gtg acc acc aac gag aca gct cgc ttc gac gtc tat	1546
Lys Asp Ile Lys Val Thr Thr Asn Glu Thr Ala Arg Phe Asp Val Tyr	
485 490 495	
gtc gcg gtt cct tac ggt gac ctc gcc gga ccc gac tac ggc gag ttc	1594
Val Ala Val Pro Tyr Gly Asp Leu Ala Gly Pro Asp Tyr Gly Glu Phe	
500 505 510	
gcg ggc agc tac gtg agg ctg gcg cat agg atg aag gga agc gac ggg	1642
Ala Gly Ser Tyr Val Arg Leu Ala His Arg Met Lys Gly Ser Asp Gly	
515 520 525 530	
acc gaa aag cag ggc ccc aag aag aag gga aaa ctc aag ctg ggt att	1690
Thr Glu Lys Gln Gly Pro Lys Lys Lys Gly Lys Leu Lys Leu Gly Ile	
535 540 545	
acg ccg ctg ctc gag gac atc gat gct gag gac gcc gac aag ttg gtg	1738
Thr Pro Leu Leu Glu Asp Ile Asp Ala Glu Asp Ala Asp Lys Leu Val	
550 555 560	
gtc acc ctg gtt ctc cgc act ggg agc gtc acc gtg ggg gga gtt tcc	1786
Val Thr Leu Val Leu Arg Thr Gly Ser Val Thr Val Gly Gly Val Ser	
565 570 575	
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atc aat ctc ctg cag aca gat tct acc gcc gcc atc taaatgatgg	1832
Ile Asn Leu Leu Gln Thr Asp Ser Thr Ala Ala Ile	
580 585 590	

cctcggatca cagcttctcc ccgcttaagt tggagtgate gattactggt gctgctttct 1892
tcttccctgt cgttcttget atcttcttga tctggaacga tccttcaata attagggcat 1952
gacagtagtc gtcgcccgat cccatagtga cgtgttggtc tcaacagctg tacatgtgac 2012
gttatggtgt gactatatat ttattgagg tcaccttgt ttctttctta aaaaaaaaaa 2072
aaaaaa 2078

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<211> 590
<212> PRT
<213> banana

<400> 22
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Leu Leu Gln Arg Glu Arg Ser Arg Arg Arg Arg Leu His Val Pro Gly
20 25 30
Val Thr Cys Arg Gln Gly Ser Asn Gly Asp Arg Arg Asp Ala Ala Pro
35 40 45
Gln Gln Gln Ser Pro Pro Leu Leu Asp Arg Arg Asp Met Leu Leu Gly
50 55 60
Leu Gly Gly Leu Tyr Gly Val Thr Ala Gly Pro Lys Val Leu Ala Ala
65 70 75 80
Pro Ile Met Pro Pro Asp Leu Ser Lys Cys Tyr Pro Ala Thr Ala Pro
85 90 95
Ala Leu Asp Asn Lys Cys Cys Pro Pro Tyr Asp Pro Gly Glu Thr Ile
100 105 110
Ser Glu Tyr Ser Phe Pro Ala Thr Pro Leu Arg Val Arg Arg Pro Ala
115 120 125
His Ile Val Lys Asp Asp Gln Glu Tyr Met Asp Lys Tyr Lys Glu Ala
130 135 140

Val Arg Arg Met Lys Asn Leu Pro Ala Asp His Pro Trp Asn Tyr Tyr
145 150 155 160

Gln Gln Ala Asn Ile His Cys Gln Tyr Cys Asn Tyr Ala Tyr His Gln
165 170 175

Gln Asn Thr Asp Asp V l Pro Ile Gln Val His Phe Ser Trp Ile Phe
180 185 190

Leu Pro Trp His Arg Tyr Tyr Leu His Phe Tyr Glu Arg Ile Leu Gly
195 200 205

Lys Leu Ile Asp Asp Asp Thr Phe Thr Ile Pro Phe Trp Asn Trp Asp
210 215 220

Thr Lys Asp Gly Met Thr Phe Pro Ala Ile Phe Gln Asp Ala Ala Ser
225 230 235 240

Pro Leu Tyr Asp Pro Arg Arg Asp Gln Arg His Val Lys Asp Gly Lys
245 250 255

Ile Leu Asp Leu Lys Tyr Ala Tyr Thr Glu Asn Thr Ala Ser Asp Ser
260 265 270

Glu Ile Ile Arg Glu Asn Leu Cys Phe Ile Gln Lys Thr Phe Lys His
275 280 285

Ser Leu Ser Leu Ala Glu Leu Phe Met Gly Asp Pro Val Arg Ala Gly
290 295 300

Glu Lys Glu Ile Gln Glu Ala Asn Gly Gln Met Glu Val Ile His Asn
305 310 315 320

Ala Ala His Met Trp Val Gly Glu Pro Asp Gly Tyr Lys Glu Asn Met
325 330 335

Gly Asp Phe Ser Thr Ala Ala Arg Asp Ser Val Phe Phe Cys His His
340 345 350

Ser Asn Val Asp Arg Met Trp Asp Ile Tyr Arg Asn Leu Arg Gly Asn
355 360 365

Arg Val Glu Phe Glu Asp Asn Asp Trp Leu Asp Ser Thr Phe Leu Phe
370 375 380

His Asp Glu Asn Glu Gln Leu Val Lys Val Lys Met Ser Asp Cys Leu
385 390 395 400

Asn Pro Thr Lys Leu Arg Tyr Thr Phe Glu Gln Val Pro Leu Pro Trp
405 410 415

Leu Gly Lys Ile Asn Cys Gln Lys Thr Ala Glu Thr Lys Ser Lys Ala
420 425 430

Thr Thr Glu Leu Ser Leu Thr Arg Val Asn Glu Phe Gly Thr Thr Ala
435 440 445

Gln Ala Leu Asp Ala Ser Asn Pro Leu Arg Val Ile Val Ala Arg Pro
450 455 460

Lys Lys Asn Arg Lys Lys Lys Glu Lys Gln Glu Lys Val Gly Val Ile
465 470 475 480

Gln Ile Lys Asp Ile Lys Val Thr Thr Asn Glu Thr Ala Arg Phe Asp
485 490 495

Val Tyr Val Ala Val Pro Tyr Gly Asp Leu Ala Gly Pro Asp Tyr Gly
500 505 510

Glu Phe Ala Gly Ser Tyr Val Arg Leu Ala His Arg Met Lys Gly Ser
515 520 525

Asp Gly Thr Glu Lys Gln Gly Pro Lys Lys Lys Gly Lys Leu Lys Leu
530 535 540

Gly Ile Thr Pro Leu Leu Glu Asp Ile Asp Ala Glu Asp Ala Asp Lys
545 550 555 560

Leu Val Val Thr Leu Val Leu Arg Thr Gly Ser Val Thr Val Gly Gly
565 570 575

Val Ser Ile Asn Leu Leu Gln Thr Asp Ser Thr Ala Ala Ile
580 585 590

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<211> 900

<212> DNA

<213> banana

<220>

<221> CDS

<222> (13)..(729)

<400> 23

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Met Trp Thr Val Trp Lys Lys Leu His Gly Asp Lys Pro

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gag ttc gtc gac cag gag tgg ctc gag tct gaa ttc acc ttc tac gac			99
Glu Phe Val Asp Gln Glu Trp Leu Glu Ser Glu Phe Thr Ph Tyr Asp			
15	20	25	
gag aat gtg cgc ctg cgc agg atc aag gtg cgc gac gtg ttg aac ata			147
Glu Asn Val Arg Leu Arg Arg Ile Lys Val Arg Asp Val Leu Asn Ile			
30	35	40	45
gac aaa ctc agg tac cgg tac gaa gac atc gac atg cca tgg ctc gct			195
Asp Lys Leu Arg Tyr Arg Tyr Glu Asp Ile Asp Met Pro Trp Leu Ala			
50	55	60	
gca cgt ccc aag cct tcc gtt cac cct aag atc gcg cgc gac ata ttg			243
Ala Arg Pro Lys Pro Ser Val His Pro Lys Ile Ala Arg Asp Ile Leu			
65	70	75	
aag aag cgt aat ggc gaa ggc gta ctg aga atg ccc ggc gaa acg gat			291
Lys Lys Arg Asn Gly Glu Gly Val Leu Arg Met Pro Gly Glu Thr Asp			
80	85	90	
cgt tca caa ctc tcc gaa gat ggt agc tgg aca ctg gac aag agc atc			339
Arg Ser Gln Leu Ser Glu Asp Gly Ser Trp Thr Leu Asp Lys Ser Ile			
95	100	105	
acc gtg agg gtt gac agg cca agg atc aac agg aca ggg caa gaa aaa			387
Thr Val Arg Val Asp Arg Pro Arg Ile Asn Arg Thr Gly Gln Glu Lys			
110	115	120	125
gag gaa gaa gag gag atc tta ttg gtc tac gga atc gat act aag aga			435
Glu Glu Glu Glu Glu Ile Leu Leu Val Tyr Gly Ile Asp Thr Lys Arg			
130	135	140	
agc aga ttc gtc aaa ttc gat gtg ttc atc aac gtc gtc gac gaa acc			483
Ser Arg Phe Val Lys Phe Asp Val Phe Ile Asn Val Val Asp Glu Thr			
145	150	155	
gtg ctg aac cca aag tcg agg gag ttc gca ggg acc ttc gtc aat ctc			531
Val Leu Asn Pro Lys Ser Arg Glu Phe Ala Gly Thr Phe Val Asn Leu			
160	165	170	
cac cac gtc tcg agg acg aaa agc cat gag gat ggc ggc gtg ggt tcg			579
His His Val Ser Arg Thr Lys Ser His Glu Asp Gly Gly Val Gly Ser			
175	180	185	
aag atg aaa agc cac ctt aag ctc ggt ata tcg gaa ctt ttg gaa gac			627
Lys Met Lys Ser His Leu Lys Leu Gly Ile Ser Glu Leu Leu Glu Asp			

190 195 200 205

ctc gag gca gac gaa gat gat tgc atc tgg gtg aca ctg gtg cca aga 675
 Leu Glu Ala Asp Glu Asp Asp Cys Ile Trp Val Thr Leu Val Pro Arg
 210 215 220

ggc ggc acg ggg gtc aac acc acc gta gac ggc gtc cgg atc gac tac 723
 Gly Gly Thr Gly Val Asn Thr Thr Val Asp Gly Val Arg Ile Asp Tyr
 225 230 235

atg aag tagtgaaccg gcacgccgct cctcccctcc ccatcagaag tggataata 779
 Met Lys

tttatattgg atcgaggctc gtggtatctt ttgataagag taagttccat aaatttagaa 839

gaagaatcat gttctttatt tatattaaat caatgtgatt tgtccaaaaa aaaaaaaaaa 899

a 900

<210> 24
 <211> 239
 <212> PRT
 <213> banana

<400> 24
 Met Trp Thr Val Trp Lys Lys Leu His Gly Asp Lys Pro Glu Phe Val
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Asp Gln Glu Trp Leu Glu Ser Glu Phe Thr Phe Tyr Asp Glu Asn Val
 20 25 30

Arg Leu Arg Arg Ile Lys Val Arg Asp Val Leu Asn Ile Asp Lys Leu
 35 40 45

Arg Tyr Arg Tyr Glu Asp Ile Asp Met Pro Trp Leu Ala Ala Arg Pro
 50 55 60

Lys Pro Ser Val His Pro Lys Ile Ala Arg Asp Ile Leu Lys Lys Arg
 65 70 75 80

Asn Gly Glu Gly Val Leu Arg Met Pro Gly Glu Thr Asp Arg Ser Gln
 85 90 95

Leu Ser Glu Asp Gly Ser Trp Thr Leu Asp Lys Ser Ile Thr Val Arg
 100 105 110

Val Asp Arg Pro Arg Ile Asn Arg Thr Gly Gln Glu Lys Glu Glu Glu
115 120 125

Glu Glu Ile Leu Leu Val Tyr Gly Ile Asp Thr Lys Arg Ser Arg Phe
130 135 140

Val Lys Phe Asp Val Phe Ile Asn Val Val Asp Glu Thr Val Leu Asn
145 150 155 160

Pro Lys Ser Arg Glu Phe Ala Gly Thr Phe Val Asn Leu His His Val
165 170 175

Ser Arg Thr Lys Ser His Glu Asp Gly Gly Val Gly Ser Lys Met Lys
180 185 190

Ser His Leu Lys Leu Gly Ile Ser Glu Leu Leu Glu Asp Leu Glu Ala
195 200 205

Asp Glu Asp Asp Cys Ile Trp Val Thr Leu Val Pro Arg Gly Gly Thr
210 215 220

Gly Val Asn Thr Thr Val Asp Gly Val Arg Ile Asp Tyr Met Lys
225 230 235

<210> 25

<211> 1522

<212> DNA

<213> pineapple

<220>

<221> CDS

<222> (3)..(1271)

<400> 25

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1 5 10 15

gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt cct tgg cac 95
Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His
20 25 30

cgg ttc tac ctc tac tcc aac gag cgc ata ctc ggg aaa ctt atc ggc 143
Arg Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly
35 40 45

gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg ccg ggg ggc 191

Asp Asp Thr Ph	Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly	
50	55	60
atg cag ttc ccg tct atc tac acg gac cct tca tcc tcg cta tat gac	239	
Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp		
65	70	75
aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att gac ctc gac	287	
Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp		
80	85	90 95
tac aat ggc acc gat cct acc ttc tcc cct gaa gaa cag att aac cac	335	
Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His		
100	105	110
aac ctc gcc gtc atg tac cga cag gtg ata tcc agt gga aag aca cca	383	
Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro		
115	120	125
gag ctg ttt atg ggc tca gcg tac cgc gcc ggt gac cag cct gac ccc	431	
Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro		
130	135	140
ggc gca ggc tct gta gag cag aag ccg cac ggc ccg gtg cat gtg tgg	479	
Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp		
145	150	155
aca ggt gat cgc aac cag ccc aat cgc gaa gac atg ggc acg ctc tac	527	
Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr		
160	165	170 175
tcg gcg gcg tgg gac ccc gtc ttc ttc gca cac cac ggc aac atc gac	575	
Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp		
180	185	190
cgc atg tgg tac gtg tgg agg aac ctt ggc ggc aag cac cgc aac ttc	623	
Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe		
195	200	205
acc gac ccc gac tgg ctc aac gcg tcc ttc ctg ttc tat gat gag aat	671	
Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn		
210	215	220
gcg cag ctc gtc cgt gtt aaa gta aaa gac tgc tta gag gcc gac gca	719	
Ala Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu Ala Asp Ala		
225	230	235

atg cgg tac aca tac cag gat gta gag atc ccg tgg ctc aaa gca aag	767
Met Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Ala Lys	
240 245 250 255	
ccg acg cca aag agc gcc cta cag aag ata aag agc aag gta tcg acg	815
Pro Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys Val Ser Thr	
260 265 270	
ctg aag gca aca cca agg ggg acg acg act acc aca gca gag act aca	863
Leu Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Thr Ala Glu Thr Thr	
275 280 285	
ttt ccg gtg gtg ctg gat aag ccg gtg agt gca aca gtg gct aga ccg	911
Phe Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val Ala Arg Pro	
290 295 300	
aag gcc agg agg agt ggg aag gag aag gaa gaa gag gag gag gtg ttg	959
Lys Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu Glu Glu Val Leu	
305 310 315	
gtg gtg gag gga atc gag ttg gag aag gac gtg ttc gtg aag ttt gat	1007
Val Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val Lys Phe Asp	
320 325 330 335	
gtg tat ata aac tcg ccg gag cac gaa ggg gtg ggg ccg gag gcg agt	1055
Val Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro Glu Ala Ser	
340 345 350	
gag ttc gca ggg agc ttc gtc cac gtg cca cac aag cac aag aag gcg	1103
Glu Phe Ala Gly Ser Phe Val His Val Pro His Lys His Lys Lys Ala	
355 360 365	
aag aag ggg aag gag atg gcc agg atg aac aca agg ctt aag ctc ggg	1151
Lys Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu Lys Leu Gly	
370 375 380	
ata acg gac ctg ctc gag gac atc gcc gct gag gac gac gag agc gtg	1199
Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp Glu Ser Val	
385 390 395	
ctc atc acg ctc gtg ccc agg agc ggc aag gga atg gtg aag gtt gga	1247
Leu Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val Lys Val Gly	
400 405 410 415	
ggg cta agg att gat ttc tcc aag tgatgagcat attgtgaaga gaaaatttgc	1301
Gly Leu Arg Ile Asp Phe Ser Lys	
420	

atttaccgco ctatagaato gaaaaattgc gtatatgtcc cattattgtt ttttttattc 1361
 ttcaagcgta ttcagaataa gagttgcgtg catgcacgca tgcagccatg ttgttgtagt 1421
 cgtatgtgg ggtatgtttg gatcagggat aatgatgtga accttgaatt aattattaca 1481
 ctctgagaat aaattagaga gtttattatg caaaaaaaaa a 1522

<210> 26
 <211> 423
 <212> PRT
 <213> pineapple

<400> 26
 His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asp
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 Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His Arg
 20 25 30
 Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp
 35 40 45
 Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met
 50 55 60
 Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp Lys
 65 70 75 80
 Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp Tyr
 85 90 95
 Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His Asn
 100 105 110
 Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro Glu
 115 120 125
 Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro Gly
 130 135 140
 Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp Thr
 145 150 155 160
 Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr Ser
 165 170 175

Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp Arg	180	185	190
Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe Thr	195	200	205
Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn Ala	210	215	220
Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu Ala Asp Ala Met	225	230	235 240
Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Ala Lys Pro	245	250	255
Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys Val Ser Thr Leu	260	265	270
Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Thr Ala Glu Thr Thr Phe	275	280	285
Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val Ala Arg Pro Lys	290	295	300
Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu Glu Glu Val Leu Val	305	310	315 320
Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val Lys Phe Asp Val	325	330	335
Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro Glu Ala Ser Glu	340	345	350
Phe Ala Gly Ser Phe Val His Val Pro His Lys His Lys Lys Ala Lys	355	360	365
Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu Lys Leu Gly Ile	370	375	380
Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp Glu Ser Val Leu	385	390	395 400
Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val Lys Val Gly Gly	405	410	415
Leu Arg Ile Asp Phe Ser Lys	420		

<210> 27
 <211> 875
 <212> DNA
 <213> pineapple

<220>
 <221> CDS
 <222> (3)..(875)

<400> 27
 ac aac aaa cca gtg cct ggt tta ggt gta ttc act atg gcc acc etc 47
 Asn Lys Pro Val Pro Gly Leu Gly Val Phe Thr Met Ala Thr Leu
 1 5 10 15
 tct aaa cta gct tcc cca acc aat aac acc tcc act ctc ccc gct ccc 95
 Ser Lys Leu Ala Ser Pro Thr Asn Asn Thr Ser Thr Leu Pro Ala Pro
 20 25 30
 tcc ttt gca tgc tcc ttc tct cac caa aag ctt cac cac cac ctt cct 143
 Ser Phe Ala Cys Ser Phe Ser His Gln Lys Leu His His His Leu Pro
 35 40 45
 ctc ccc tgt agg ggt ccc aaa cca ccc cgt cat aag atc tca tgc aaa 191
 Leu Pro Cys Arg Gly Pro Lys Pro Pro Arg His Lys Ile Ser Cys Lys
 50 55 60
 tct aag gag caa caa gag aat gcc gac aag cct gcg ggc cgc atc gac 239
 Ser Lys Glu Gln Gln Glu Asn Ala Asp Lys Pro Ala Gly Arg Ile Asp
 65 70 75
 cgc cgc gac cta ctc ctg ggc etc ggc ggg ctt tac ggt gcc acc act 287
 Arg Arg Asp Leu Leu Leu Gly Leu Gly Gly Leu Tyr Gly Ala Thr Thr
 80 85 90 95
 ggg etc ggc etc aac cgt cga gcg gcc gcc gcc cct atc ctg gct ccc 335
 Gly Leu Gly Leu Asn Arg Arg Ala Ala Ala Pro Ile Leu Ala Pro
 100 105 110
 gac etc tca act tgt ggg ccg cct gcc gac etc cct gcc tcc gcc cga 383
 Asp Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala Ser Ala Arg
 115 120 125

ccg aca gtt tgc tgc ccg cca tac caa tcc acc atc atc gtc ttc aag 431
 Pro Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile Val Phe Lys
 130 135 140

ctc ccc ccg cga tct gct ccg ctt cgc gtc cgg cct gcg gcc cac ttg 479
 Leu Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala Ala His Leu
 145 150 155

gtt gac gcc gac tac ctg gcc aag tat aag aag gcg gtc gag ctc atg 527
 Val Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val Glu Leu Met
 160 165 170 175

agg gcc ctg ccg gcc gac gac ccg cgc aac ttc gta cag caa gcg aaa 575
 Arg Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln Gln Ala Lys
 180 185 190

gtg cac tgt gcg tac tgc gac ggc gcg tac gac caa atc ggc ttc ccc 623
 Val His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro
 195 200 205

gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt cct tgg cac 671
 Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His
 210 215 220

cgg ttc tac ctc tac ttc aac gag cgc ata ctc ggg aaa ctt atc ggt 719
 Arg Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly
 225 230 235

gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg ccg ggg ggc 767
 Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly
 240 245 250 255

atg cag ttc ccg tct atc tac aca gac cct tca tcc tcg cta tat gac 815
 Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp
 260 265 270

aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att gac ctc gac 863
 Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp
 275 280 285

tac aat ggc aca 875
 Tyr Asn Gly Thr
 290

<210> 28

<211> 291

<212> PRT

<213> pineapple

<400> 28

Asn Lys Pro Val Pro Gly Leu Gly Val Phe Thr Met Ala Thr Leu Ser
1 5 10 15

Lys Leu Ala Ser Pro Thr Asn Asn Thr Ser Thr Leu Pro Ala Pro Ser
20 25 30

Phe Ala Cys Ser Phe Ser His Gln Lys Leu His His His Leu Pro Leu
35 40 45

Pro Cys Arg Gly Pro Lys Pro Pro Arg His Lys Ile Ser Cys Lys Ser
50 55 60

Lys Glu Gln Gln Glu Asn Ala Asp Lys Pro Ala Gly Arg Ile Asp Arg
65 70 75 80

Arg Asp Leu Leu Leu Gly Leu Gly Gly Leu Tyr Gly Ala Thr Thr Gly
85 90 95

Leu Gly Leu Asn Arg Arg Ala Ala Ala Ala Pro Ile Leu Ala Pro Asp
100 105 110

Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala Ser Ala Arg Pro
115 120 125

Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile Val Phe Lys Leu
130 135 140

Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala Ala His Leu Val
145 150 155 160

Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val Glu Leu Met Arg
165 170 175

Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln Gln Ala Lys Val
180 185 190

His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asp
195 200 205

Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His Arg
210 215 220

Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp
225 230 235 240

Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met
245 250 255

Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp Lys
260 265 270

Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp Tyr
275 280 285

Asn Gly Thr
290

<210> 29

<211> 2057

<212> DNA

<213> lettuce

<220>

<221> CDS

<222> (16) .. (1842)

<400> 29

gaccacccat agatg atg gct tct ctc gcc ttg tct agt ctt ccc acc tcc 51
Met Ala Ser Leu Ala Leu Ser Ser Leu Pro Thr Ser
1 5 10

acc aca acc aaa aaa ccc tta ttt tcc aaa aca tcc tcg cat gtt aag 99
Thr Thr Thr Lys Lys Pro Leu Phe Ser Lys Thr Ser Ser His Val Lys
15 20 25

cca ttc cat cgc ttc aaa gtt tca tgc aat gca ccc gct gat aac aat 147
Pro Phe His Arg Phe Lys Val Ser Cys Asn Ala Pro Ala Asp Asn Asn
30 35 40

gac aaa acc gtc aat aat tct gat acc cca aag ctc ata cta ccc aaa 195
Asp Lys Thr Val Asn Asn Ser Asp Thr Pro Lys Leu Ile Leu Pro Lys
45 50 55 60

aca cca ctt gaa acg cag aac gta gac agg aga aac ttg ctt ctg gga 243
Thr Pro Leu Glu Thr Gln Asn Val Asp Arg Arg Asn Leu Leu Leu Gly
65 70 75

ctc gga ggt ctc tac ggc gct gcc aac ttg acg acc att ccg tca gcc 291
Leu Gly Gly Leu Tyr Gly Ala Ala Asn Leu Thr Thr Ile Pro Ser Ala
80 85 90

ttt ggc att ccc atc gct gct cca gac aat att tca gac tgt gtt gct 339
Phe Gly Ile Pro Ile Ala Ala Pro Asp Asn Ile Ser Asp Cys Val Ala
95 100 105

gcg act tca aac cta agg aac agc aaa gac gct ata agg gga cta gcg 387
Ala Thr Ser Asn Leu Arg Asn Ser Lys Asp Ala Ile Arg Gly Leu Ala
110 115 120

tgt tgt cct ccg gtg ctt tca aca aac aaa cca atg gat tac gtc ctt 435
Cys Cys Pro Pro Val Leu Ser Thr Asn Lys Pro Met Asp Tyr Val Leu
125 130 135 140

cct tca aac cct gtg att cgt gtt cga cca gct gca cag aaa gcc act 483
Pro Ser Asn Pro Val Ile Arg Val Arg Pro Ala Ala Gln Lys Ala Thr
145 150 155

gcc gat tac act gct aag tat caa caa gca att caa gcc atg aag gat 531
Ala Asp Tyr Thr Ala Lys Tyr Gln Gln Ala Ile Gln Ala Met Lys Asp
160 165 170

ctc ccc gag gac cac cca cat agc tgg aag caa caa ggc aag att cac 579
Leu Pro Glu Asp His Pro His Ser Trp Lys Gln Gln Gly Lys Ile His
175 180 185

tgt gct tat tgc aac ggt ggt tac aat caa gaa caa agt ggt tac ccg 627
Cys Ala Tyr Cys Asn Gly Gly Tyr Asn Gln Glu Gln Ser Gly Tyr Pro
190 195 200

aat tta caa ctt cag att cac aac tca tgg ctc ttc ttt cct ttc cac 675
Asn Leu Gln Leu Gln Ile His Asn Ser Trp Leu Phe Phe Pro Phe His
205 210 215 220

cgg tgg tac ctc tat ttc tac gag aag ata ttg ggg aag ttg att aat 723
Arg Trp Tyr Leu Tyr Phe Tyr Glu Lys Ile Leu Gly Lys Leu Ile Asn
225 230 235

gat cca act ttc gct cta cct tac tgg aac tgg gat aac cct act gga 771
Asp Pro Thr Phe Ala Leu Pro Tyr Trp Asn Trp Asp Asn Pro Thr Gly
240 245 250

atg gtt att cct gcc atg ttc gaa cag aac agc aaa act aac tct ctg 819
Met Val Ile Pro Ala Met Phe Glu Gln Asn Ser Lys Thr Asn Ser Leu
255 260 265

ttt gac cct tta agg gat gcg aaa cac ctc cca cct tct atc ttt gat 867
Phe Asp Pro Leu Arg Asp Ala Lys His Leu Pro Pro Ser Ile Phe Asp
270 275 280

gtt gaa tat gct ggt gca gac act ggt gcc act tgt ata gac cag ata 915
Val Glu Tyr Ala Gly Ala Asp Thr Gly Ala Thr Cys Ile Asp Gln Ile

285	290	295	300	
gcc att aat ctg tct tca atg tac aga cag atg gtc acc aac tcc act				963
Ala Ile Asn Leu Ser Ser Met Tyr Arg Gln Met Val Thr Asn Ser Thr				
305		310	315	
gat aca aaa cga ttc ttc ggt ggc gaa ttt gta gct gga aat gac cct				1011
Asp Thr Lys Arg Phe Phe Gly Gly Glu Phe Val Ala Gly Asn Asp Pro				
320	325		330	
ctt gcg agc gag ttc aac gta gct ggg acc gta gaa gct ggg gtt cac				1059
Leu Ala Ser Glu Phe Asn Val Ala Gly Thr Val Glu Ala Gly Val His				
335	340		345	
act gcg gct cac cgc tgg gtg ggt aat tct agg atg gcc aac agc gaa				1107
Thr Ala Ala His Arg Trp Val Gly Asn Ser Arg Met Ala Asn Ser Glu				
350	355		360	
gac atg ggg aac ttc tac tcc gca gga tat gat cct ctc ttt tac gtc				1155
Asp Met Gly Asn Phe Tyr Ser Ala Gly Tyr Asp Pro Leu Phe Tyr Val				
365	370	375	380	
cac cat gcg aat gtc gac agg atg tgg caa atc tgg aaa gat att gac				1203
His His Ala Asn Val Asp Arg Met Trp Gln Ile Trp Lys Asp Ile Asp				
385	390		395	
aag aag aca cac aag gat ccg acc tct ggc gac tgg cta aat gca tca				1251
Lys Lys Thr His Lys Asp Pro Thr Ser Gly Asp Trp Leu Asn Ala Ser				
400	405		410	
tac gtg ttt tac gat gag aat gaa aat ctt gta cgt gtc tac aac cga				1299
Tyr Val Phe Tyr Asp Glu Asn Glu Asn Leu Val Arg Val Tyr Asn Arg				
415	420		425	
gac tgt gta gac att aat cgg atg gga tat gac tac gaa agg tca gca				1347
Asp Cys Val Asp Ile Asn Arg Met Gly Tyr Asp Tyr Glu Arg Ser Ala				
430	435		440	
atc cca tgg atc cgt agt cgg ccg act gca cat gcg aag ggg gcg aac				1395
Ile Pro Trp Ile Arg Ser Arg Pro Thr Ala His Ala Lys Gly Ala Asn				
445	450	455	460	
gtt gct gct aag tct gct gga atc gtg cag aag gtg gag gat atc gta				1443
Val Ala Ala Lys Ser Ala Gly Ile Val Gln Lys Val Glu Asp Ile Val				
465	470		475	
ttc ccg ctg aag tta aac aag ata gtg aag gtt cta gtg aag agg cca				1491
Phe Pro Leu Lys Leu Asn Lys Ile Val Lys Val Leu Val Lys Arg Pro				

480	485	490	
gct aca aac agg acc aag gag gga aag gag aaa gca aat g g ctg ttg			1539
Ala Thr Asn Arg Thr Lys Glu Gly Lys Glu Lys Ala Asn Glu Leu Leu			
495	500	505	
ttc gtg aat gga atc acg ttt gat gct gag cgg ttt cta aag att gac			1587
Phe Val Asn Gly Ile Thr Phe Asp Ala Glu Arg Phe Leu Lys Ile Asp			
510	515	520	
gtg ttt gtc aac gac gtc gac gat gga att cag acc acc gct gct gat			1635
Val Phe Val Asn Asp Val Asp Asp Gly Ile Gln Thr Thr Ala Ala Asp			
525	530	535	540
agt gag ttt gct ggt agt ttc gca cag ttg cca cat aac cat ggc gac			1683
Ser Glu Phe Ala Gly Ser Phe Ala Gln Leu Pro His Asn His Gly Asp			
545	550	555	
aag atg ttt atg agg agt ggg gca gcg ttc ggg atc acg gag ctc ttg			1731
Lys Met Phe Met Arg Ser Gly Ala Ala Phe Gly Ile Thr Glu Leu Leu			
560	565	570	
gaa gac att gaa gct gaa ggt gat gac tct gtt gtt gtg aca ttg gtg			1779
Glu Asp Ile Glu Ala Glu Gly Asp Asp Ser Val Val Val Thr Leu Val			
575	580	585	
ccg aga aca ggg tgt gat gaa gta act att ggc gag atc aag att cag			1827
Pro Arg Thr Gly Cys Asp Glu Val Thr Ile Gly Glu Ile Lys Ile Gln			
590	595	600	
ctg gtt ccc att gtt taaagtctat tgaagtaatg cattttcaat tgtcattagt			1882
Leu Val Pro Ile Val			
605			
atgcatgggt acgtaaatct gttcgctgtc tggtracga ggatttttga tgttctcgta			1942
accaaataat aaggattgtc attccatggt tggaaatcgtg taaccgcagg catgcatatg			2002
tttgattggt atttttactt gaagcacttc tgttttagta aaaaaaaaaa aaaaa			2057

<210> 30

<211> 609

<212> PRT

<213> lettuce

<400> 30

Met	Ala	Ser	Leu	Ala	Leu	Ser	Ser	Leu	Pro	Thr	Ser	Thr	Thr	Thr	Lys	1	5	10	15
Lys	Pro	Leu	Phe	Ser	Lys	Thr	Ser	Ser	His	Val	Lys	Pro	Phe	His	Arg	20	25	30	
Phe	Lys	Val	Ser	Cys	Asn	Ala	Pro	Ala	Asp	Asn	Asn	Asp	Lys	Thr	Val	35	40	45	
Asn	Asn	Ser	Asp	Thr	Pro	Lys	Leu	Ile	Leu	Pro	Lys	Thr	Pro	Leu	Glu	50	55	60	
Thr	Gln	Asn	Val	Asp	Arg	Arg	Asn	Leu	Leu	Leu	Gly	Leu	Gly	Gly	Leu	65	70	75	80
Tyr	Gly	Ala	Ala	Asn	Leu	Thr	Thr	Ile	Pro	Ser	Ala	Phe	Gly	Ile	Pro	85	90	95	
Ile	Ala	Ala	Pro	Asp	Asn	Ile	Ser	Asp	Cys	Val	Ala	Ala	Thr	Ser	Asn	100	105	110	
Leu	Arg	Asn	Ser	Lys	Asp	Ala	Ile	Arg	Gly	Leu	Ala	Cys	Cys	Pro	Pro	115	120	125	
Val	Leu	Ser	Thr	Asn	Lys	Pro	Met	Asp	Tyr	Val	Leu	Pro	Ser	Asn	Pro	130	135	140	
Val	Ile	Arg	Val	Arg	Pro	Ala	Ala	Gln	Lys	Ala	Thr	Ala	Asp	Tyr	Thr	145	150	155	160
Ala	Lys	Tyr	Gln	Gln	Ala	Ile	Gln	Ala	Met	Lys	Asp	Leu	Pro	Glu	Asp	165	170	175	
His	Pro	His	Ser	Trp	Lys	Gln	Gln	Gly	Lys	Ile	His	Cys	Ala	Tyr	Cys	180	185	190	
Asn	Gly	Gly	Tyr	Asn	Gln	Glu	Gln	Ser	Gly	Tyr	Pro	Asn	Leu	Gln	Leu	195	200	205	
Gln	Ile	His	Asn	Ser	Trp	Leu	Phe	Phe	Pro	Phe	His	Arg	Trp	Tyr	Leu	210	215	220	
Tyr	Phe	Tyr	Glu	Lys	Ile	Leu	Gly	Lys	Leu	Ile	Asn	Asp	Pro	Thr	Phe	225	230	235	240
Ala	Leu	Pro	Tyr	Trp	Asn	Trp	Asp	Asn	Pro	Thr	Gly	Met	Val	Ile	Pro	245	250	255	

Ala Met Phe Glu Gln Asn Ser Lys Thr Asn Ser Leu Ph Asp Pro Leu
260 265 270

Arg Asp Ala Lys His Leu Pro Pro Ser Ile Phe Asp Val Glu Tyr Ala
275 280 285

Gly Ala Asp Thr Gly Ala Thr Cys Ile Asp Gln Ile Ala Ile Asn Leu
290 295 300

Ser Ser Met Tyr Arg Gln Met Val Thr Asn Ser Thr Asp Thr Lys Arg
305 310 315 320

Phe Phe Gly Gly Glu Phe Val Ala Gly Asn Asp Pro Leu Ala Ser Glu
325 330 335

Phe Asn Val Ala Gly Thr Val Glu Ala Gly Val His Thr Ala Ala His
340 345 350

Arg Trp Val Gly Asn Ser Arg Met Ala Asn Ser Glu Asp Met Gly Asn
355 360 365

Phe Tyr Ser Ala Gly Tyr Asp Pro Leu Phe Tyr Val His His Ala Asn
370 375 380

Val Asp Arg Met Trp Gln Ile Trp Lys Asp Ile Asp Lys Lys Thr His
385 390 395 400

Lys Asp Pro Thr Ser Gly Asp Trp Leu Asn Ala Ser Tyr Val Phe Tyr
405 410 415

Asp Glu Asn Glu Asn Leu Val Arg Val Tyr Asn Arg Asp Cys Val Asp
420 425 430

Ile Asn Arg Met Gly Tyr Asp Tyr Glu Arg Ser Ala Ile Pro Trp Ile
435 440 445

Arg Ser Arg Pro Thr Ala His Ala Lys Gly Ala Asn Val Ala Ala Lys
450 455 460

Ser Ala Gly Ile Val Gln Lys Val Glu Asp Ile Val Phe Pro Leu Lys
465 470 475 480

Leu Asn Lys Ile Val Lys Val Leu Val Lys Arg Pro Ala Thr Asn Arg
485 490 495

Thr Lys Glu Gly Lys Glu Lys Ala Asn Glu Leu Leu Phe Val Asn Gly
500 505 510

Ile Thr Phe Asp Ala Glu Arg Phe Leu Lys Ile Asp Val Phe Val Asn
515 520 525

Asp Val Asp Asp Gly Ile Gln Thr Thr Ala Ala Asp Ser Glu Phe Ala
530 535 540

Gly Ser Phe Ala Gln Leu Pro His Asn His Gly Asp Lys Met Phe Met
545 550 555 560

Arg Ser Gly Ala Ala Phe Gly Ile Thr Glu Leu Leu Glu Asp Ile Glu
565 570 575

Ala Glu Gly Asp Asp Ser Val Val Val Thr Leu Val Pro Arg Thr Gly
580 585 590

Cys Asp Glu Val Thr Ile Gly Glu Ile Lys Ile Gln Leu Val Pro Ile
595 600 605

Val

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gcgaattctt yytnccntty mymg

24

<210> 32
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gcgaattcga tccnacntty gckttnc

28

<210> 33
<211> 26
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gcgaattcaa ygtngaymgn atgtgg

26

<210> 34

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34

gcgaattctn caytgygcnt aytg

24

<210> 35

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 35

gcgaattctt nccntwytg aaytgga

27

<210> 36

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 36

gcctgcagcc acatnckrtc nacrtt

26

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 37

gcctgcagtt ytcrtcttag aa

22

<210> 38

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 38

gactcgagtc gacatcgatt tttttttttt ttttt

35

<210> 39

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

atatcacctg tcggtacatg acggc

25

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

gtgccattgt agtcgaggtc aatca

25

<210> 41

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

ccagtgccctg gtttaggtgt attcac

26

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
<400> 42
tgctgttctg ttcgaacatg gcag

24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
<400> 43
tatacaagtg gcaccagtgt ctgc

24

<210> 44
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
<400> 44
ccgcattgtg gatgacttcc atctg

25

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
<400> 45
ccagaatggg atggtgaagg tgctg

25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 46

cgctgggtgg gtaattctag gatg

24

<210> 47

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 47

agtcattccac aatgcggcgc acatg

25

<210> 48

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 48

gttgctcttc ttaggctcgg cttac

25

<210> 49

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 49

gactcgagtc gacatcg

17